

GLUTRNA^{GLN} AMIDOTRANSFERASE - A NOVEL ESSENTIAL TRANSLATIONAL COMPONENT

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03818/0200029

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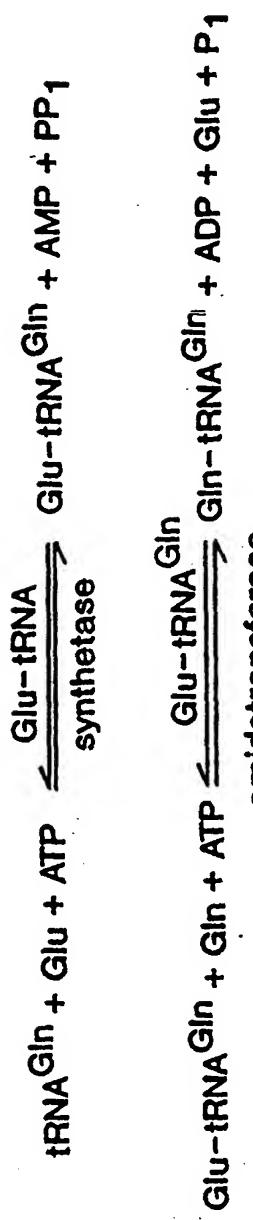


FIG. 1

pABC (pBluescript KS-ABC, 6.4 kb, Ap^r)

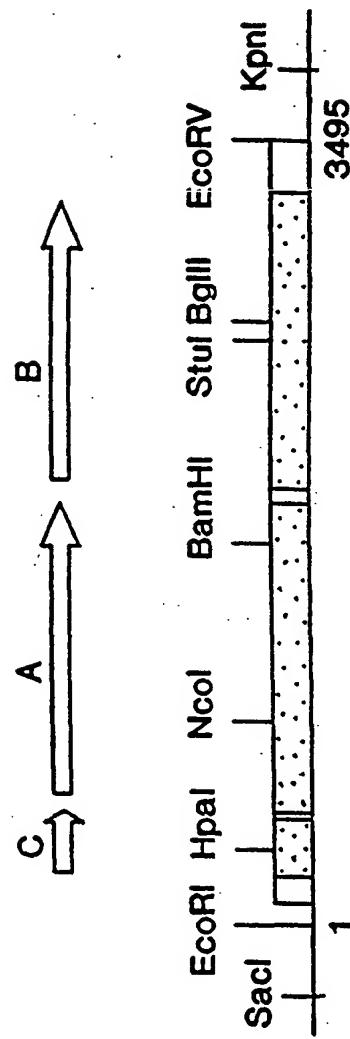


FIG. 2

GLUTR_{NA}^{GLN} AMIDOTRANSFERASE - A NOVEL ESSENTIAL TRANSLATIONAL COMPONENT

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FIGURE 3A

1
 1 **GAATTC**GATC CTGTCTCAAG GCGTTTGTG GCTTTAAAGG GCTTGTGTTT
 (EcoRI)

51 GATATGATCA GTATTATATG ACTTAACGGA GAAATATGTG GAGGTGGATC
 C
 START→

101 ATATGTCACG AATTTCAATA GAAGAAGTAA AGCACGTTGC GCACCTTGCA

151 AGACTTGCAG TTACTGAAGA AGAAGCAAAA ATGTTCACTG AACAGCTCGA

201 CAGTATCATT TCATTTGCCG AGGAGCTTAA TGAGGTTAAC ACAGACAATG

251 TGGAGCCTAC AACTCACGTG CTGAAAATGA AAAATGTCAT GAGAGAAGAT

301 GAAGCGGGTA AAGGTCTTCC GGTTGAGGAT GTCATGAAAA ATGCGCCTGA

351 CCATAAAAGAC GGCTATATTG GTGTGCCATC AATTCTGGAC TAAAGGAGGG
 A
 START→

401 ACACAAGAAT GTCATTATTT GATCATAAAA TCACAGAATT AAAACAGCTC

451 ATACATAAAA AAGAGATTAA GATTTCTGAT CTGGTTGATG AATCTTATAAA

501 ACGCATCCAA GCGGTTGATG ATAAGGTACA AGCCTTTTG GCATTAGATG

551 AAGAAAGACG CGCGGCATAC GCGAAGGAGC TTGATGAGGC GGTTGACGGC

601 CGTTCTGAGC ACGGTCTTCT TTTCGGTATG CCGATCGGCG TAAAAGATAA

651 TATCGTAACA AAAGGGCTGC GCACAACATG CTCCAGCAAA ATTCTCGAAA

701 ACTTTGATCC GATTTACGAT GCTACTGTCG TTCAGCGCCT TCAAGACGCT

751 GAAGCGGTCA CAATCGGAAA ACTGAACATG GACGAATTGCG CCATGGGTC

801 ATCTACAGAA AACTCAGCTT ACAAGCTGAC GAAAAACCCCT TGGAACCTGG

851 ATACAGTTCC CGGCGGTCA AGCGGCGGAT CTGCAGCTGC GGTTGCTGCG

901 GGAGAAAGTTC CGTTTCTCT TGGATCTGAC ACAGGCGGCT CCATCCGTCA

951 GCCGGCATCT TTCTGCGGCG TTGTCGGATT AAAACCTACA TACGGACGTG

1001 TATCTCGTTA CGGCCTGGTC GCATTTGCGT CTTCATTGGA CCAAATCGGA

1051 CCGATTACAC GTACGGTGA GGATAACGCG TTTTTACTTC AAGCGATTTG

1101 CGGCGTAGAC AAAATGGACT CTACGAGTGC AAATGTGGAC GTGCCTGATT

1151 TTCTTTCTTC ATTAACGTC GACATCAAAG GACTGAAAAT CGCCGTTCCG

1201 AAAGAAATACC TTGGTGAAGG TGTCGGCAAA GAAGCGAGAG AATCTGTCTT

1251 GGCAGCGCTG AAAGTCCTTG AAGGTCTCGG CGCTACATGG GAAGAAGTGT

1301 CTCTTCCGCA CAGTAAATAC GCGCTTGCGA CATATTACCT GCTGTCATCT

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FIGURE 3B

1351	TCTGAAGCGT	CAGCGAACCT	TGCACGCTT	GACGGCATCC	GCTACGGCTA
1401	CCGCACAGAC	AACGCGGATA	ACCTGATCGA	CCTTTACAAG	CAAACCGCG
1451	CTGAAGGTTT	CGGAAATGAA	GTCAAACGCC	GCATCATGCT	CGGAACGTTT
1501	GCTTTAAGCT	CAGGCTACTA	CGATGCGTAC	TACAAAAAAG	CGCAAAAAGT
1551	GCGTACGTTG	ATTAAGAAGG	ATTCGAGGA	CGTATTTGAA	AAATATGATG
1601	TTATTGTTGG	ACCGACTACA	CCGACACCTG	CGTTTAAAAT	CGGTGAAAAC
1651	ACGAAGGATC	CGCTCACAAAT	GTACGCAAAC	GATATCTTAA	CGATTCCGGT
1701	CAACCTTGCG	GCGTACCGGG	AATCAGGTGC	CATGCGGTTA	GCAGACGGAC
1751	TTCCGCTCGG	CCTGCAAATC	ATCGGAAAAC	ACTTTGATGA	AGCACTGTAT
1801	ACCGCGTTGC	TCATGCAATT	GAACAAGCAA	CAGACCATCA	TAAAGCAAAA
		B			
		START \rightarrow			
1851	CCTGAACTGT	AAGGGGTGAA	AAGAATTGAA	CTTGAAACG	GTAATCGGAC
1901	TTGAAGTCCA	CGTTGAGTTA	AAAACAAAAT	CAAAAATTTT	CTCAAGCTCT
1951	CCAACGCCAT	TCGGCGCGGA	GGCGAATACG	CAGACAAGCG	TTATTGACCT
2001	CGGATATCCG	GGCGTCCTGC	CTGTTCTGAA	CAAAGAAGCC	GTTGAATTG
2051	CAATGAAAGC	CGCTATGGCG	CTCAACTGTG	AGATCGCAAC	GGATACGAAG
2101	TTTGACCGCA	AAAACTATTT	CTATCCTGAC	AACCCGAAAG	CGTATCAGAT
2151	TTCTCAATT	GATAAGCCAA	TCGGCGAAAA	CGGCTGGATC	GAAATTGAAG
2201	TCGGCGGCAA	AACAAAACGC	ATCGGCATCA	CGCGCCTTCA	TCTTGAAGAG
2251	GATGCCGGAA	AACTGACGCA	TACGGGCGAC	GGCTATTCTC	TTGTTGACTT
2301	CAACCGTCAA	GGAACGCCGC	TTGTTGAGTN	CGTATCAGAG	CCGGACATCC
2351	GCACGCCGGA	AGAACNGTAC	GCATATCTG	AAAAGCTGAA	ATCCATCATC
2401	CAATATACAG	GCGTTTCTGA	CTGTAAAATG	GAAGAAGGCT	CACTTCGCTG
2451	TGACGCCAAT	ATCTCTCTTC	GTCCGATCGG	CCAAGAGGAA	TTCCGGCACAA
2501	AAACAGAATT	AAAAAACTTG	AACTCCTT	CGTTTGTCA	AAAAGGCCTT
2551	GAGCATGAAG	AAAAACGCCA	GGAGCAGGTT	CTTCTTTCCG	GCTTCTTCAT
2601	CCAGCAAGAA	ACTCGCCGTT	ATGATGAAGC	AACGAAGAAA	ACCATTCTTA
2651	TGCGTGTCAA	AGAGGGATCT	GACGACTACC	GTTACTTCCC	AGAGCCAGAT

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FIGURE 3C

2701	CTAGTCGAGC	TCTACATTGA	TGATGAATGG	AAGGAACGCG	TAAAAGCAAG
2751	CATTCCCTGAG	CTTCCGGATG	AGCGCCGCAA	GCGTTATATC	GAAGAGCTTG
2801	GCTTCGCTGC	ATATGACGCA	ATGGTTCTGA	CGCTGACAAA	AGAAATGGCT
2851	GATTTCCTCG	AAGAAACCGT	TCAAAAAGGC	GCTGAAGCTA	AACAAGCGTC
2901	TAACCTGGCTG	ATGGGTGAAG	TGTCAGCTTA	CCTAAACGCA	GAACAAAAAG
2951	AGCTTGCCGA	TGTTGCCCTG	ACACCTGAAG	GCCTTGCCGG	CATGATCAAA
3001	TTGATTGAAA	AAGGAACCAT	TTCTTCTAAG	ATCGCGAAGA	AAGTGTAA
3051	AGAATTGATT	GAAAAAGGCG	GCGACGCTGA	GAAGATTGTG	AAAGAGAAAG
3101	GCCTTGTCA	GATTTCCTGAC	GAAGGCGTGC	TTCTGAAGCT	TGTCACTGAG
3151	GCGCTTGACA	ACAATCCTCA	ATCAATCGAA	GACTTTAAAA	ACGGAAAAGA
3201	CCGGCGCGATC	GGCTTCCTAG	TCGGACAGAT	TATGAAAGCG	TCCAAAGGAC
3251	AAGCCAACCC	GCCGATGGTC	AACAAAATTG	TGCTTGAAGA	AATTAAAAAA
3301	CGCTAATAAA	AAAGCAGCCC	TTAGAGGCTG	CTTTTTTTAT	GGTCAAATTG
3351	AGATAAAAGAC	AAGATGAGGG	CCCGAAGCCT	TTCAACTTCT	TTGTCGTTGG
3401	TTCCGGCCAA	ATTGGACAGC	ATGCCTTTAT	AATCGGCTTG	CGCGGTTTAT
3451	CCTGAGTCAA	TTCTTCCTCG	ATAAGATAAG	TGACACGGTG	3495 (ECORV) ATATC